

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:36 ; Search time 299.73 Seconds

(without alignments)
23.463 Million cell updates/sec

Title: US-09-331-631A-21_COPY_32_91

Perfect score: 343

Sequence: 1 TENPCAQRCLQSCQEPDDL.....DTGATNQRHPERTGRGP 60

Scoring table: BLOSUM62

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

```

1: SPTRMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	23.0	62	10 Q9M402	Q9M402 glycine max
2	75	21.9	411	5 P91419	P91419 caenorhabd
3	71.5	20.8	388	5 O44606	O44606 caenorhabd
4	70	20.4	221	5 O16446	O16446 caenorhabd
5	70	20.4	378	5 O27383	O27383 caenorhabd
6	69.5	20.3	625	10 Q9SP13	Q9SP13 macadamia
7	69	20.1	1187	2 Q49549	Q49549 mycoplasma
8	68.5	20.0	666	10 Q9SP14	Q9SP14 macadamia
9	68.5	20.0	1513	5 O17970	O17970 caenorhabd
10	67.5	19.7	438	5 O16502	O16502 caenorhabd
11	67.5	19.7	445	5 O16511	O16511 caenorhabd
12	66.5	19.4	287	4 Q9UD01	Q9UD01 homo sapien
13	66	19.2	242	5 O19919	O19919 caenorhabd
14	66	19.2	388	5 O16500	O16500 caenorhabd
15	66	19.2	388	5 O16501	O16501 caenorhabd
16	64.5	18.8	240	13 Q91A12	Q91A12 heterodonlu
17	64.5	18.8	666	10 Q9SP15	Q9SP15 macadamia
18	64	18.7	1036	4 Q9NZV1	Q9NZV1 homo sapien
19	63.5	18.5	593	10 Q9SEW4	Q9SEW4 juglans reg

20	63.5	18.5	1587	4 Q9Y6N6	Q9Y6N6 homo sapien
21	63	18.4	572	5 O19594	O19594 caenorhabd
22	63	18.4	4123	4 O75851	O75851 homo sapien
23	62.5	18.2	703	1 O26748	O26748 methanobact
24	62.5	18.2	1315	5 Q9VA01	Q9VA01 drosophila
25	62	18.1	224	10 Q38746	Q38746 atriplex nu
26	62	18.1	328	13 Q9YHX3	Q9YHX3 brachydanio
27	62	18.1	4458	13 Q93291	Q93291 fuqu rubrip
28	61.5	17.9	894	5 Q24925	Q24925 eupyrima sc
29	61	17.8	151	10 Q43656	Q43656 triticum ae
30	61	17.8	181	10 P93360	P93360 nicotiana t
31	61	17.8	547	10 Q24145	Q24145 nicotiana t
32	61	17.8	697	5 Q9V011	Q9V011 drosophila
33	61	17.8	728	5 O19182	O19182 caenorhabd
34	61	17.8	838	4 Q9Y6A5	Q9Y6A5 homo sapien
35	61	17.8	838	4 Q9UM01	Q9UM01 homo sapien
36	61	17.8	1028	11 Q9JTL0	Q9JTL0 mus musculu
37	61	17.8	1568	4 Q95785	Q95785 homo sapien
38	60.5	17.6	263	5 O18283	O18283 caenorhabd
39	60.5	17.6	328	5 Q9TY01	Q9TY01 caenorhabd
40	60.5	17.6	375	5 Q20002	Q20002 caenorhabd
41	60.5	17.6	532	5 Q9VCC7	Q9VCC7 drosophila
42	60.5	17.6	761	4 Q9UHI2	Q9UHI2 homo sapien
43	60.5	17.6	1631	4 Q9Y6U6	Q9Y6U6 homo sapien
44	60	17.5	96	5 Q9U512	Q9U512 manduca sex
45	60	17.5	201	5 Q9U807	Q9U807 ptychodera

ALIGNMENTS

RESULT	1	ALIGNMENTS
Q9M402	Q9M402	PRELIMINARY; PRT; 62 AA.
AC	Q9M402;	
DT	01-OCY-2000 (TREMBLrel. 15, Created)	
DT	01-OCY-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-OCY-2000 (TREMBLrel. 15, Last annotation update)	
DE	ALPHA, ALPHA'-TYPE BETA-CONGLYCININ (FRAGMENT).	
GN	BCSP	
OS	Glycine max (Soybean).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1;	
OC	Fabales; Fabaceae; Papilionoideae; Glycine.	
OX	NCBI_TaxID=3847;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	De Amicis F.;	
RL	Thesis (1998), University of udine, DPVTA.	
DR	EMBL; AJ276118; CAB83040.1; -.	
FT	NON_TER	
FT	62	
SQ	SEQUENCE 62 AA: 7158 MW; 10690D53F7700443 CRC64;	

Query Match 23.0%; Score 79; DB 10; Length 62;
Best local Similarity 43.8%; Pred. No. 0.0093;
Matches 14; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

OY	2	ENPCAQRCLQSCQEPDDLKQACESRCKLE	33
DB	31	EIRPNKCLQSCSERSDYNQACHRCNLK	62
RESULT	2		
ID	P91419	PRELIMINARY;	PRT; 411 AA.
AC	P91419;		

DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE CODED FOR Br C. ELEGANS CDNA YK115A6.5.
GN T01D1.6.
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloiderinae; *Caenorhabditis*.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsay T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lighting J., Lloyd C., McMurry A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlmann P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans.;
RL Nature 368:32-38(1994).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RC BRADSHAW H., WOHLMANN P.;
RA Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RC WATERSTON R.;
RA Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
RN EMBL: U08455; AAB37867.1; --
SQ SEQUENCE 411 AA; 44675 MW; 599DAC9DCFA81382 CRC64;

	Query Match	21.9%	Score 75;	DB 5;	Length 411;	
	Best Local Similarity	37.0%	Pred. No. 0.16;			
	Matches 17;	Conservative	8;	Mismatches 17;	Indels 4;	Gaps 3.
Dd	3 NPCAORCLQSCQGEPPDDLKORACESRCRKLEYDPRCVYDTG-ATNQ 47 1 - - - - - : : : : : - : - - - - : : : 216 NTCONSCLNTCCQQOQOQPVQO--CQSSCDQ-SCQPQCATPSPGSAYNQ 258					
RESULT	3					
ID	044606	PRELIMINARY;	PRT;	388 AA.		
AC	044606;					
DT	01-JUN-1998 (TREMBLrel. 06, Created)					
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)					
DT	01-OCT-2000 (TREMBLrel. 15, last annotation update)					
DE	R09B5.5 PROTEIN.					
GN	R09B5.5.					
OS	Caeenorhabditis elegans.					
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;					
OC	Rhabditidae; Peloiderinae; Caenorhabditis.					
OX	NCBI_Taxid=6239;					
[1]						
RP	SEQUENCE FROM N.A.					
RC	STRAIN-BRISTOL NZ;					
RX	MEDLINE=94150718; PubMed=7906398;					
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,					
RA	Balford J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,					
RA	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,					
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,					
RA	Jones M., Keshaw J., Kirsten J., Laister N., Latreille P.,					
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,					
RA	Parsons J., Percy C., Riften G., Roopra A., Saunders D., Showkneen R.,					

RA Shaldon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Wainstock L., Wilkinson-Sproat J., Wohlmann P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.
 RT elegans*.".
 RL Nature 368:32-38(1994).
 RN 12)
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Sammons L., Wohlmann P., Bauer C., Antoniou B., Wilson R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN 13)
 RN SEQUENCE FROM N.A.
 RP STRAIN=BRISTOL N2;
 RC
 RA Materston R.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 QO EMBL: AF039046; AAB94214.1; --
 SQ SEQUENCE 388 AA; 11440 MW; EA9C34AAAEABFE46 CRC64;

	Query Match	20.8%	Score 71.5	DB 5,	Length 388;
	Best Local Similarity	32.1%;	Pred No 0.4;		
	Matches 17;	Conservative 7;	Mismatches 22;	Indels 7;	Gaps 2
QY	5 CAQCLQSG--QQEPDILKQKACSEBCKTLELYDPRCVDTGATNQHHPERT	55			
	:: :: :: :: :: :: :: ::				
Db	196 CQDCCOSSCTQDDCPANOCNSAGNSQCNSI-----CQDAQAQTQOYYNNONSNT	243			
	:: :: :: :: :: :: :: ::				

RESULT	4			
Q0	016446			
DN	016446	PRELIMINARY;	PRT;	221 AA.
AC	016446;			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DE	C54F6.6 PROTEIN.			
GN	C54F6.6			
OS	Caenorhabditis elegans.			
OC	Eukaryotes; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
PN	11			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RX	MEDLINE=94150718; Pubmed=7906398;			
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton A., Dear S., Du Z., Dublin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kerstjens J., Kirsten J., Laister N., Latreille P., Raes J., Ramesh S., Rastbach A., Rost B., Searles J., Seeger A., Smith J., Smith J., Lloyd C., McMurry A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken A., Rikopa A., Saunders D., Shownkeen R., Smalton N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin R., Vaughan K., Waterston R., Watson A., Wellstock L., Wilkinson-Spoat J., Wohlbrand P.;			
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";			
RT	Nature 368:32-38(1994).			
RL	12			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RC	Geisel C., Bradshaw H.;			
RL	Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RA	Waterston R.;			
RL	Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.			
DN	EMBL: AF016447; AAB65837.1; -; FC9040399EA3EB87C CRC64;			
Q0	SEQUENCE 221 AA; 25043 MW; FC9040399EA3EB87C CRC64;			

Query Match	20.4%;	Score 70;	DB 5;	Length 221;
Best Local Similarity	29.6%;	Pred. NO. 0.37;		
Matches 16;	Conservative 7;	Mismatches 15;	Indels 16;	Gaps 2;

```

QY      3  NPCAQRCLSGCQEQEPDDLKQKACESRCKLEY-----DPRCYVD 41
      1 1 1 : : : : : : : : : : : : : : : : : : : : : : : : :
DB     165  NNCAPKCFSSSPDKKDENVLK-CETTKAKLRTTMEEDDAKFSPDFENCNQACVYD 21

```

RESULT	5	
Q27383		
ID	Q27383	PRELIMINARY;
NO	027383	PRT; 378 AA

DT	01-JUN-1998	(TREMBLrel. 06, Created)
DT	01-JUN-1998	(TREMBLrel. 06, last sequence update)
DT	01-JUN-1998	(TREMBLrel. 06, last annotation update)
DE	HYPOTHETICAL 40-7 KDA PROTEIN R09F10.2 IN CHROMOSOME X PRECURSOR.	
GN	R09F10.2 AND R09F10.7.	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae	
OC	Rhabditidae; Pelodierinae; Caenorhabditis.	
OX	NCBI_TaxId=6239;	
OX	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-BRISTOL N2.	
RA	Couch J.	
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: BELONGS TO FAMILY UPE.	
DR	EMBL: U64859; AACG9090.1; -	
DR	EMBL: U64859; AACG9096.1; -	
DR	MORMPEP: R09F10.2; CE07436.	
DR	MORMPEP: R09F10.7; CE07441.	
KM	Hypothetical protein; signal.	
FT	SIGNAL	
FT	CHAIN	POTENTIAL.
FT	19	378
Q	SEQUENCE	378 AA; 40663 MW; E36BA16BEF3A77610 CRC54;

Query Match	20.4%	Score 70;	DB 5;	Length 378;
Best Local Similarity	37.8%;	Pred. NO. 0.6;		
Matches 14; Conservative	6;	Mismatches 11;	Indels 6;	Gaps 2

QY 5 CAQKRLQSCQDEP-----DDLKQKACESCRTKLEYDP 36
 . | | | | | : | : | : | : | : |
 Db 84 CQQSCRQQCQAPAVSQCPMCQQQCCQSQCTPM-YNP 119

RESULT	6
Q9SPL3	
ID	Q9SPL3
PRELIMINARY;	PRT;
	625 AA

DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).
GN AMP2.

US *Macadamia integrifolia* (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
NCBI_TaxID=60698;

RT globulin protein in Macadamia integrifolia?;

DR	EMBL:	AF161865:	AAD54246.1:	-
NR	Protein:	U_01000(1999):		
DR	HSSP:	P02853:	2PHL	
DR	INTERPRO:	IPR001113:	-	
DR	PFAM:	PF00546:	Seedstore_7s:	1.
FT	NON_TER			
DR	SEQUENCE	625 AA:	73386 MW:	415808A89D370296 CRC64

Query Match	20.3%	Score 69.5;	DB 10;	length 625;
Best Local Similarity	30.0%	Pred. No. 1.1;		
Matches , 12;	Conservative 10;	Mismatches 11;	Indels 7;	Gaps 1;

DQY 5 CAQRICDSCQQEPPDDLKOK-----ACESRCKLEIDPR 37
| : | : | : | : | : | :
Db 61 CQRCAICEEEFYNNRRDPQQYEQCRCRKQRRETEPR 100

RESULT 7
Q49549
ID Q49549
AC Q49549.
PRELIMINARY;
PRT; 1187 AA.

DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE REPEAT REGIONS IN POTENTIAL METAL BINDING PROTEIN GENE REGION
 OS Mycoplasma hyorhinis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2100;
 RN [1]
 RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=GDL1;
 RC MEDLINE=95014025; PubMed=7928953;
 RA Deng G., McIntosh M.A.;
 RT "An amplifiable DNA region from the Mycoplasma hyorhinis genome
 RL J. Bacteriol. 176:5929-5937(1994).
 DR EMBL: L11447; AAA62228.1;
 QQ SEQUENCE 11187 AA: 15027 MW: 66A62AE5B0EDE93E CRC64;

Query Match	20.1%;	Score 69;	DB 2;	Length 1187;
Best Local Similarity	28.6%;	Pred. NO. 2.2;		
Matches	20;	Conservative	12;	Mismatches 22; Indels 16; Gaps 5

OY 1 TEPPCAQRRLQ-----CQGEPPDLKQKAC---BSRCKTLEYDPRCV-----YDT---GATN 46
|| : | : : : || : : || :
Db 403 TEERHC--ECTESTGCCENEECEEFACDCSEHCEGVDETQAQLDCNTQAADTKVCGCTQ 460

```
QY      47 QHPPGERTR 56
        ::||| |
Db      461 EQHPTCEECK 470
```

RESULT	8	
Q9SPL4		
ID	Q9SPL4	PRELIMINARY;
		PRT; 666 AA.

DT	01-MAY-2000	(Tremblurel, 13, Created)
DT	01-MAY-2000	(Tremblurel, 13, Last sequence update)
DT	01-OCT-2000	(Tremblurel, 15, Last annotation update)
DE	VICILIN PRECURSOR.	
GN	AMP2.	

05 *Macadamia integrifolia* (Macadamia nut).
0C Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
0C Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
0X NCBI_TaxID=60698;

RT
RT
RT
RT
RC
RC
RP
SEQUENCE FROM N.A.
TISSUE=NUT KERNEL:
Marcus J.P., Coulter K.C., Green J.L., Manners J.M.;
"A family of antimicrobial peptides is produced by processing of a 7S
globulin protein in *Macadamia integrifolia*.";

KL PLANT J. 0:0-0(1999).
 DR EMBL: AF161884: AAD4245.1; -.
 DR HSSP: P02853; PRTL.
 DR INTERPRO: IPR001113; -.
 DR PFAM: PF00546; Seedstore 7s; 1.
 SQ SEQUENCE 666 AA; 7843 MW; 0ECA228B710F8A7B CRC64

Query Match	20.3%	Score 69.5;	DB 10;	length 625;
Best Local Similarity	30.0%	Pred. No. 1.1;		
Matches , 12;	Conservative 10;	Mismatches 11;	Indels 7;	Gaps 1;

DQY 5 CAQRICDSCQQEPDDLKQ-----ACESRCKLEIDPR 37
|:::|::|::||::|:
Db 61 CQRCAICEEEHYNRORDPQQYECCQCRCRRRETEPR 100

RESULT 7
Q49549
ID Q49549
AC Q49549.
PRELIMINARY;
PRT; 1187 AA.

DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE REPEAT REGIONS IN POTENTIAL METAL BINDING PROTEIN GENE REGION
 OS Mycoplasma hyorhinis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2100;
 RN [1]
 RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=GDL1;
 RC MEDLINE=95014025, PubMed=7928953;
 RA Deng G., McIntosh M.A.;
 RT "An amplifiable DNA region from the Mycoplasma hyorhinis genome
 RL J. Bacteriol. 176:5929-5937(1994).
 DR EMBL: L11447, AAA62228.1;
 QQ SEQUENCE 11187 AA: 15027 MW: 66A62AE5B0DE93E CRC64;

Query Match	20.1%;	Score 69;	DB 2;	Length 1187;
Best Local Similarity	28.6%;	Pred. NO. 2.2;		
Matches 20;	Conservative 12;	Mismatches 22;	Indels 16;	Gaps 5

```
OY      1 TERNCAQRRLQ-----CQGEPPDLKKQAC--BSRCTKLEYDPRV-----YDT---GATN 46
         || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    403 TEHRH--PCTESTGCCENEPCCEFEACDCSEHHCCEVDYQACLDCNTQAADTKVCGCTQ 460
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QY      47 QHPPGERTR 56
        ::||| | :
Db      461 EQHPTCEECK 470
```

RESULT	8	
Q9SPL4		
ID	Q9SPL4	PRELIMINARY;
		PRT; 666 AA.

DT	01-MAY-2000	(Tremblurel, 13, Created)
DT	01-MAY-2000	(Tremblurel, 13, Last sequence update)
DT	01-OCT-2000	(Tremblurel, 15, Last annotation update)
DE	VICILIN PRECURSOR.	
GN	AMP2.	

05 *Macadamia integrifolia* (Macadamia nut).
0C Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
0C Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
0X NCBI_TaxID=60698;

RT
RT
RT
RT
RC
RC
RP
SEQUENCE FROM N.A.
TISSUE=NUT KERNEL:
Marcus J.P., Coulter K.C., Green J.L., Manners J.M.;
"A family of antimicrobial peptides is produced by processing of a 7S
globulin protein in *Macadamia integrifolia*.";

KL PLANT J. 0:0-0(1999).
 DR EMBL: AF161884: AAD4245.1; -.
 DR HSSP: P02853; PRTL.
 DR INTERPRO: IPR001113; -.
 DR PFAM: PF00546; Seedstore 7s; 1.
 SQ SEQUENCE 666 AA; 7843 MW; 0ECA228B710F847B CRC64

```

Query Match Summary          20.0%: Score 68.5; DB 10; Length 666;
Best Local Similarity       30.0%: Pred. No. 1.5;
Matches          12: Conservative 10; Mismatches 11; Indels 7; Gaps 1

OY      5 CAORCLOSCQEPDDLKOK-----ACESRCKTLEYDPR 37
      1 :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB      102 CORCKEICEEEYENRDRDPOQOYEOCCERCORHETTER 141

RESULT  9
ID      017970      PRELIMINARY:      PRT: 1513 AA.
AC      017970:
DT      01-JAN-1998 (TREMBLrel. 05, Created)
DT      01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE      M0269.1 PROTEIN.
GN      M0269.1.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Matthews L.;
RL      Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE-94150718; PubMed=7906398;
RA      Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
RA      Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA      Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA      Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA      Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA      Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
RA      Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA      Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA      Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA      Watson A., Weinstock L., Wilkinson-Spoat J., Wohldman P.;
RT      *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT      elegans.
RL      Nature 368:32-38(1994).
DR      EMBL; 281573; CAB04625.1; -.
DR      HSP; 046655; ICJH.
SQ      SEQUENCE 1513 AA; 161578 MW; 10BCB4287BA282E5 CRC64;

Query Match          20.0%: Score 68.5; DB 5; Length 1513;
Best Local Similarity 28.8%: Pred. No. 3.2;
Matches          15: Conservative 9; Mismatches 11; Indels 17; Gaps 3

OY      4 PCOAOCLOSCQOE-----PDDIKKACESCTKLEYPRCYVDGAT 45
      1 :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
DB      405 PCQPCLOSCLEOHIIQPOVYVTLPPCIPQ--CQPC-----EPQCIQETTTT 449

RESULT  10
ID      016502      PRELIMINARY:      PRT: 438 AA.
AC      016502:
DT      01-JAN-1998 (TREMBLrel. 05, Created)
DT      01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE      C03A7.8 PROTEIN.
GN      C03A7.8.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN=BRISTOL NZ;
RC
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RX MEDLINE=94150718; PubMed=7906398
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berts M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latteille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Greco T., Bradshaw H., Elliott G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF016451; AAB55995.1; -
SQ SEQUENCE 438 AA; 47502 MW; 835C4F68BECF510B1 CRC64;

Query Match 19.7%; Score 67.5; DB 5; Length 438;
Best Local Similarity 33.3%; Pred. No. 1.4;
Matches 15; Conservative 7; Mismatches 16; Indels 7; Gaps 2;

OY 5 CAORCLQSC--QDEPDDLKQKACGSRCKLEYDPRCVYDTGATNQ 47
Db 201 CQOQCCSCVQOQOOPSTOCEPACNTQCSDI-----CQOTAGATQ 240

RESULT 11
O16511 PRELIMINARY; PRT; 445 AA.
AC O16511;
DT 01-JAN-1998 (TREMBLrel. 05, created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE C0347.14 PROTEIN.
GN C0347.14
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabditidae;
OC Rhabdilitae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berts M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latteille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Greco T., Bradshaw H., Elliott G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases
DR EMBL: AF016451; AAB66007.1; -
SQ SEQUENCE 445 AA; 48202 MW; A65C08DC136BADA CXC64;

Query Match Similarity 19.7%; Score 67.5; DB 5; Length 445;
Best Local Similarity 33.3%; Pred. No. 1.4;
Matches 15; Conservative 7; Mismatches 16; Gaps 2

QY 5 CAQRCLQSC--QQEPDDLKQACACESRCTKLEYDPRCYVDGTATNQ 47
| : | | | : | : | : | : |
Db 201 CQQQCQSVCVQQQQPSTQCEPACNTQCSDI-----CQTAAQTQQ 240

RESULT 12	
Q9UDQ1	
ID Q9UDQ1	PRELIMINARY;
Q9UDQ1	PRT; 287 AA

OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TaxID=9606;		
XN		
DE	SEMAPHORIN III PRECURSOR (FRAGMENT).	
DT	1-JUN-2000	(TREMBL). 14, last annotation update)
DD		
DT	01-MAY-2000	(TREMBL). 13, last sequence update)
DT	01-MAY-2000	(TREMBL). 13, last sequence update)
DT		
OS	Homo sapiens (Human).	
CC		

RP SEQUENCE FROM N.A.
RA MEDLINE=95063792; PubMed=9847074;
RX Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).

RP SEQUENCE FROM N.A.
RA Holmes A., Gregory S.;
RT "The sequence of Homo sapiens PAC clone RP5-1060B1.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBSJ databases
RT

RN
 RP SEQUENCE FROM N.A.
 RN (17)
 RA Waterston R.H.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases
 RN [4]
 RP SEQUENCE FROM N.A.

Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases
EMBL; AC006322; AAD20933.1; -
INTEPBP0; TBP003006; -

DR	PFAM; PF00047; ig; 1.	
FT	NON_TER	1
SO	SEQUENCE	287 AA; 33548 MW; CBC66E2E944D573F CRC64;

Query Match	19.48;	Score 66.5;	DB 4;	Length 287;
Best Local Similarity	35.28;	Pred. No. 1.3;		
Matches 19; Conservative	5;	Mismatches 23;	Indels 7;	Gaps 2

QY 6 AQRCLQSQQEPPDDLKQACACESRCKLEYDPRCVYDTGATNQRHPHGERTGRQ 59
| | : || | | : : : : :
Db 26 AQPLHRC-----DIYKACAEC--LARDPYCAMDGASCSRIFFTAKRRTRRQ 72

RESULT	13	
ID	Q19919	PRELIMINARY;
	Q19919	PRT;
	Q19919	242 AA

01-JUN-1998 (TREMBLrel..06, Created)
DT
01-JUN-1998 (TREMBLrel..06, Last sequence update)
DT
01-JUN-1998 (TREMBLrel..06, Last annotation update)
DT
DE HYPOTHETICAL 26.2 KDA PROTEIN F3IA3.1 IN CHROMOSOME X
FN F3IA3.1.

OS *Caenorhabditis elegans*.
 CC Eukaryota; Metazoa; Nematoda; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 H32

RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Murray J., Le T., T. J.
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases
-1- STRAIN-BRISTOL N2; MURRAY J., LE T., T. J.

DR	EMBL; U58742; AAB36856.1; -;
DR	MORPEP; F3IA3.1; CE07158.
KW	Hypothetical protein; Transmembrane.
FT	TRANSMEM 3 23 POTENTIAL.
SQ	SEQUENCE 242 AA; 2613 MW; C/D5996BD0829317 CAC64;

Query Match	19.24;	Score 66;	DB 5;	Length 242;
Best Local Similarity	43.33;	Pred. No. 1.2;		
Matches 13;	Conservative 3;	Mismatches 12;	Indels 2;	Gaps 1;

QY 2 ENPCAQRCLQSCQOEPPDDLKQKACESRCK 31
| | | | | : : | | | | |
Db 175 EPQCQSCQCCVCVQQQSMQ--CASACTK 202

RESULT	14	
ID	016500	PRELIMINARY;
	016500	PRT; 388 AA.

DT 01-JAN-1998 (TREMblrel.05, Created)
DT 01-JAN-1998 (TREMblrel.05, Last sequence update)
DT 01-NOV-1998 (TREMblrel.08, Last annotation update)
DE C03A7.4 PROTEIN.
NN C03A7.4

05 *Caenorhabditis elegans*.
06 *Caenorhabditis elegans*.
07 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitia; Rhabditoidae.
08 Rhabditidae; Peloderinae; Caenorhabditis.
09 NCBI_TaxID=6239;
10
11

RX MEDLINE=94150718; PubMed-7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RAF Bondfield T., Burton D., Connors T., Coulson J.,
RC STRAIN-BRISTOL N2;
RP SCIENCE FROM N.A.

RA Parsons J, Dervic C, Rifkin J, Rogers A, Saunders D, Chamberlain P, Jones M, Kershaw J, Kirsten J, Laister N, Latreille P, RA Lightning J, Lloyd C, McMurtry A, Mortimore B, O'Callaghan M, RA Gardner A, Green P, Hawkins T, Hiller L, Tier M, Johnston L, RA Craxton M, Dear S, Du Z, Durrdin R, Favella A, Fulton L, RA Jones M, Kershaw J, Kirsten J, Laister N, Latreille P, RA Lightning J, Lloyd C, McMurtry A, Mortimore B, O'Callaghan M, RA Parsons J, Dervic C, Rifkin J, Rogers A, Saunders D, Chamberlain P

RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Smailson N., Smith A., Sonnhammer E., Staeden R., Sulston J.,
 RA Smailson N., Smith A., Sonnhammer E., Staeden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.

KL mature 308:32-38 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Greco T. Bradshaw H

RL submitted (Aug-1997) to the EMBL/Genbank/DBP databases
 RN [3]
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 RC STRAIN=BRISTOL N2;
 RA Waterston R :
 AC
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RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases
DR EMBL; AF016451; AAB66001.1; -
SQ SEQUENCE 388 AA; 42139 MW; 2E20655B0B9AE492 CRC64;

Query Match	19.2%	Score	66	DB	5	Length	388
Best Local Similarity	43.8%	Pred. No.	1.9				
Matches	14	Conservative	4	Mismatches	8	Indels	6
						Gaps	1

QY 5 CAQRCLOSC-----QQEPDDLKOKACESRCT 30
 DB 317 CAPQCEQSCQOQCVOOQQAACCTACQSSCS 348

RESULT 15

016501 PRELIMINARY; PRT; 388 AA.
 ID 016501
 AC 016501;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE C03A7.7 PROTEIN.
 GN C03A7.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
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 RA Smaison N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Wellstock L., Wilkinson-Sproat J., Wohlman P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Greco T., Bradshaw H., Elliott G.,
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.,
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF016451; AAB65996.1;
 SQ SEQUENCE 388 AA; 42129 MW; 74ACA3953E0AF2A2 CRC64;

Query Match 19.2%; Score 66; DB 5; Length 388;
 Best local Similarity 43.8%; Pred. No. 1.9;
 Matches 14; Conservative 4; Mismatches 8; Indels 6; Gaps 1;
 QY 5 CAQRCLOSC-----QQEPDDLKOKACESRCT 30
 DB 317 CAPQCEQSCQOQCVOOQQAACCTACQSSCS 348

Search completed: March 1, 2001, 16:09:38
 Job time: 1582 sec